

# Yu-Chiao Chiu

## List of Publications by Year in Descending Order

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**Version:** 2024-04-29

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

51  
papers

900  
citations

18  
h-index

29  
g-index

63  
ext. papers

1,247  
ext. citations

5.8  
avg, IF

4.2  
L-index

#	Paper	IF	Citations
51	Androgen deprivation-induced elevated nuclear SIRT1 promotes prostate tumor cell survival by reactivation of AR signaling. <i>Cancer Letters</i> , <b>2021</b> , 505, 24-36	9.9	2
50	CancerSiamese: one-shot learning for predicting primary and metastatic tumor types unseen during model training. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 244	3.6	3
49	Prediction and interpretation of cancer survival using graph convolution neural networks. <i>Methods</i> , <b>2021</b> , 192, 120-130	4.6	5
48	Predicting and characterizing a cancer dependency map of tumors with deep learning. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	3
47	GDF6-CD99 Signaling Regulates Src and Ewing Sarcoma Growth. <i>Cell Reports</i> , <b>2020</b> , 33, 108332	10.6	5
46	Knock-out of Hopx disrupts stemness and quiescence of hematopoietic stem cells in mice. <i>Oncogene</i> , <b>2020</b> , 39, 5112-5123	9.2	7
45	Classification of Cancer Types Using Graph Convolutional Neural Networks. <i>Frontiers in Physics</i> , <b>2020</b> , 8,	3.9	12
44	Predicting sites of epitranscriptome modifications using unsupervised representation learning based on generative adversarial networks. <i>Frontiers in Physics</i> , <b>2020</b> , 8,	3.9	6
43	Deep learning of pharmacogenomics resources: moving towards precision oncology. <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 2066-2083	13.4	19
42	Convolutional neural network models for cancer type prediction based on gene expression. <i>BMC Medical Genomics</i> , <b>2020</b> , 13, 44	3.7	38
41	Incorporation of long non-coding RNA expression profile in the 2017 ELN risk classification can improve prognostic prediction of acute myeloid leukemia patients. <i>EBioMedicine</i> , <b>2019</b> , 40, 240-250	8.8	17
40	Predicting drug response of tumors from integrated genomic profiles by deep neural networks. <i>BMC Medical Genomics</i> , <b>2019</b> , 12, 18	3.7	71
39	CeL-ID: cell line identification using RNA-seq data. <i>BMC Genomics</i> , <b>2019</b> , 20, 81	4.5	6
38	Integrating resistance functions to predict response to induction chemotherapy in de novo acute myeloid leukemia. <i>European Journal of Haematology</i> , <b>2019</b> , 103, 417-425	3.8	4
37	Multi-omics analysis reveals the mutation and mismatch repair gene signatures associated with survival, protein expression, and copy number alterations in prostate cancer.. <i>Translational Cancer Research</i> , <b>2019</b> , 8, 1279-1288	0.3	
36	An ancestry informative marker panel design for individual ancestry estimation of Hispanic population using whole exome sequencing data. <i>BMC Genomics</i> , <b>2019</b> , 20, 1007	4.5	4
35	Analyzing Differential Regulatory Networks Modulated by Continuous-State Genomic Features in Glioblastoma Multiforme. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2018</b> , 15, 1754-1764	3	2

34	The prognostic significance of global aberrant alternative splicing in patients with myelodysplastic syndrome. <i>Blood Cancer Journal</i> , <b>2018</b> , 8, 78	7	15
33	Utilizing Cancer - Functional Gene Set - Compound Networks to Identify Putative Drugs for Breast Cancer. <i>Combinatorial Chemistry and High Throughput Screening</i> , <b>2018</b> , 21, 74-83	1.3	
32	The Clinical and Biological Implications of Early Clearance of Peripheral Blood Blasts after Induction Chemotherapy in Acute Myeloid Leukemia. <i>Blood</i> , <b>2018</b> , 132, 3991-3991	2.2	
31	GSAE: an autoencoder with embedded gene-set nodes for genomics functional characterization. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 142	3.5	24
30	scdNet: a computational tool for single-cell differential network analysis. <i>BMC Systems Biology</i> , <b>2018</b> , 12, 124	3.5	10
29	GATA2 zinc finger 1 mutations are associated with distinct clinico-biological features and outcomes different from GATA2 zinc finger 2 mutations in adult acute myeloid leukemia. <i>Blood Cancer Journal</i> , <b>2018</b> , 8, 87	7	20
28	Differential correlation analysis of glioblastoma reveals immune ceRNA interactions predictive of patient survival. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 132	3.6	13
27	Higher HOPX expression is associated with distinct clinical and biological features and predicts poor prognosis in acute myeloid leukemia. <i>Haematologica</i> , <b>2017</b> , 102, 1044-1053	6.6	19
26	Genome-wide identification of key modulators of gene-gene interaction networks in breast cancer. <i>BMC Genomics</i> , <b>2017</b> , 18, 679	4.5	2
25	The distinct biological implications of Asx1 mutation and its roles in leukemogenesis revealed by a knock-in mouse model. <i>Journal of Hematology and Oncology</i> , <b>2017</b> , 10, 139	22.4	24
24	Prognostic impacts and dynamic changes of cohesin complex gene mutations in de novo acute myeloid leukemia. <i>Blood Cancer Journal</i> , <b>2017</b> , 7, 663	7	26
23	High expression of () confers poor prognosis in acute myeloid leukemia. <i>Oncotarget</i> , <b>2017</b> , 8, 72250-72259	5.3	13
22	Prognostic significance of NPM1 mutation-modulated microRNA-mRNA regulation in acute myeloid leukemia. <i>Leukemia</i> , <b>2016</b> , 30, 274-84	10.7	21
21	A simple gene set-based method accurately predicts the synergy of drug pairs. <i>BMC Systems Biology</i> , <b>2016</b> , 10 Suppl 3, 66	3.5	8
20	Aberrant Patterns of Alternative Splicing Are Frequent Events and Harbor Prognostic Significance in Patients with Myelodysplastic Syndrome. <i>Blood</i> , <b>2016</b> , 128, 49-49	2.2	
19	Differential network analysis reveals the genome-wide landscape of estrogen receptor modulation in hormonal cancers. <i>Scientific Reports</i> , <b>2016</b> , 6, 23035	4.9	19
18	A 3-microRNA scoring system for prognostication in de novo acute myeloid leukemia patients. <i>Leukemia</i> , <b>2015</b> , 29, 1051-9	10.7	41
17	Co-modulation analysis of gene regulation in breast cancer reveals complex interplay between ESR1 and ERBB2 genes. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 7, S19	4.5	4

16	Parameter optimization for constructing competing endogenous RNA regulatory network in glioblastoma multiforme and other cancers. <i>BMC Genomics</i> , <b>2015</b> , 16 Suppl 4, S1	4.5	29
15	Analyzing differential regulatory networks modulated by continuous-state genomic features in glioblastoma multiforme <b>2015</b> ,		1
14	An mRNA expression signature for prognostication in de novo acute myeloid leukemia patients with normal karyotype. <i>Oncotarget</i> , <b>2015</b> , 6, 39098-110	3.3	31
13	The Clinical and Biological Characterization of De Novo Acute Myeloid Leukemia (AML) with GATA2 Mutation. <i>Blood</i> , <b>2015</b> , 126, 3822-3822	2.2	
12	MicroRNA-769-3p down-regulates NDRG1 and enhances apoptosis in MCF-7 cells during reoxygenation. <i>Scientific Reports</i> , <b>2014</b> , 4, 5908	4.9	24
11	DNMT3L promotes quiescence in postnatal spermatogonial progenitor cells. <i>Development (Cambridge)</i> , <b>2014</b> , 141, 2402-13	6.6	32
10	A Simple, Powerful, and Widely Applicable Micro-RNA Scoring System in Prognostication of De Novo Myeloid Leukemia Patients. <i>Blood</i> , <b>2014</b> , 124, 71-71	2.2	
9	Amplification of distant estrogen response elements deregulates target genes associated with tamoxifen resistance in breast cancer. <i>Cancer Cell</i> , <b>2013</b> , 24, 197-212	24.3	42
8	Identification of genes differentially expressed during the growth of <i>Bambusa oldhamii</i> . <i>Plant Physiology and Biochemistry</i> , <b>2013</b> , 63, 217-26	5.4	5
7	Modeling competing endogenous RNA regulatory networks in glioblastoma multiforme <b>2013</b> ,		5
6	Gene regulation, modulation, and their applications in gene expression data analysis. <i>Advances in Bioinformatics</i> , <b>2013</b> , 2013, 360678	5.5	19
5	Clinical and Prognostic Relevance of Expression of Homeodomain-Only Protein Homeobox (HOPX) in Acute Myeloid Leukemia. <i>Blood</i> , <b>2013</b> , 122, 3776-3776	2.2	1
4	A knock-in Npm1 mutation in mice results in myeloproliferation and implies a perturbation in hematopoietic microenvironment. <i>PLoS ONE</i> , <b>2012</b> , 7, e49769	3.7	18
3	miRSystem: an integrated system for characterizing enriched functions and pathways of microRNA targets. <i>PLoS ONE</i> , <b>2012</b> , 7, e42390	3.7	217
2	CancerSiamese: one-shot learning for predicting primary and metastatic tumor types unseen during model training		1
1	Assessing the Heterogeneity of Cardiac Non-myocytes and the Effect of Cell Culture with Integrative Single Cell Analysis		1